

## **RAW SEQUENCE LISTING**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/511,221  
Source: P45/10  
Date Processed by STIC: 10/24/04

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PCT

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/511,221

DATE: 10/24/2004

TIME: 09:52:21

Input Set : A:\LeA36033.ST25.txt  
 Output Set: N:\CRF4\10242004\J511221.raw

3 <110> APPLICANT: Bayer CropScience Aktiengesellschaft  
 5 <120> TITLE OF INVENTION: Helicokinin receptor  
 7 <130> FILE REFERENCE: Le A 36 033  
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/511,221  
 C--> 9 <141> CURRENT FILING DATE: 2004-10-13  
 9 <160> NUMBER OF SEQ ID NOS: 2  
 11 <170> SOFTWARE: PatentIn version 3.1  
 13 <210> SEQ ID NO: 1  
 14 <211> LENGTH: 1452  
 15 <212> TYPE: DNA  
 16 <213> ORGANISM: Heliothis virescens  
 18 <220> FEATURE:  
 19 <221> NAME/KEY: CDS  
 20 <222> LOCATION: (1)..(1452)  
 21 <223> OTHER INFORMATION:

W--> 24 <400> 1

25 atg gac act agt aca aca aat tca tca caa gat gac gac gcg gac tgg	48
26 Met Asp Thr Ser Thr Asn Ser Ser Gln Asp Asp Asp Ala Asp Trp	
27 1 5 10 15	
29 cca agg aac agt tcc att gac gag tat att ata cac aat gga act aat	96
30 Pro Arg Asn Ser Ser Ile Asp Glu Tyr Ile Ile His Asn Gly Thr Asn	
31 20 25 30	
33 gat aca ttc gaa aca ttg tac gat gtg ccg act ggt atg ata gta ctc	144
34 Asp Thr Phe Glu Thr Leu Tyr Asp Val Pro Thr Gly Met Ile Val Leu	
35 35 40 45	
37 ttg tcg ttc ctg tac ggc tca ata tca gtt ctt gcg gtg gtt ggg aac	192
38 Leu Ser Phe Leu Tyr Gly Ser Ile Ser Val Leu Ala Val Val Gly Asn	
39 50 55 60	
41 ttt ctg gtg atg tgg gtc gtg gcc acc tcg aga aga atg cag agc gtc	240
42 Phe Leu Val Met Trp Val Val Ala Thr Ser Arg Arg Met Gln Ser Val	
43 65 70 75 80	
45 aca aac tgc tac ata gcc aac tta gct tta gct gac ata gtc ata gga	288
46 Thr Asn Cys Tyr Ile Ala Asn Leu Ala Leu Ala Asp Ile Val Ile Gly	
47 85 90 95	
49 tta ttc gct gta cca ttt caa ttc caa gcc gcg ctg cta cag cgg tgg	336
50 Leu Phe Ala Val Pro Phe Gln Phe Gln Ala Ala Leu Leu Gln Arg Trp	
51 100 105 110	
53 ctg cta ccg cac ttc atg tgt ccg ttc tgc ccg ttc gtg cag gcg ctc	384
54 Leu Leu Pro His Phe Met Cys Pro Phe Cys Pro Phe Val Gln Ala Leu	
55 115 120 125	
57 agt gtc aac gtc agc gtg ttt aca ctg aca gcc atc gca gtt gac aga	432
58 Ser Val Asn Val Ser Val Phe Thr Leu Thr Ala Ile Ala Val Asp Arg	
59 130 135 140	

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61	cat	cgg	gcg	ata	atc	aca	ccg	ctc	agc	gcc	cac	act	tca	aag	cgt	att	480
62	His	Arg	Ala	Ile	Ile	Thr	Pro	Leu	Ser	Ala	His	Thr	Ser	Lys	Arg	Ile	
63	145				150					155						160	
65	gcc	aaa	gta	ata	ata	gtg	gtt	ata	tgg	ttt	ctg	gcf	ctt	tct	tta	gct	528
66	Ala	Lys	Val	Ile	Ile	Val	Val	Ile	Trp	Phe	Leu	Ala	Leu	Ser	Leu	Ala	
67					165					170						175	
69	gct	ccg	atg	gct	atg	tct	tgg	gag	gtt	atc	atg	gaa	gat	gaa	tta	gat	576
70	Ala	Pro	Met	Ala	Met	Ser	Trp	Glu	Val	Ile	Met	Glu	Asp	Glu	Leu	Asp	
71					180					185						190	
73	cca	gtt	gca	aaa	atc	tcc	tac	aaa	aag	ccg	ttt	tgt	gca	ccc	acc	gag	624
74	Pro	Val	Ala	Lys	Ile	Phe	Tyr	Lys	Lys	Pro	Phe	Cys	Ala	Pro	Thr	Glu	
75					195					200						205	
77	ttc	ggc	tcg	cat	tca	ctc	gcc	att	tat	aga	ctg	ttg	ttg	tat	gta	ttt	672
78	Phe	Gly	Ser	His	Ser	Leu	Ala	Ile	Tyr	Arg	Leu	Leu	Leu	Tyr	Val	Phe	
79					210					215						220	
81	cag	tat	gta	atc	ccg	ttg	tgt	gtg	att	acg	ttt	gcc	tac	gct	cat	atg	720
82	Gln	Tyr	Val	Ile	Pro	Leu	Cys	Val	Ile	Thr	Phe	Ala	Tyr	Ala	His	Met	
83					225					230						235	240
85	gcf	atg	aag	ctg	tgg	gga	gcf	cgc	gcc	cca	ggg	aac	gcf	cag	gag	acg	768
86	Ala	Met	Lys	Leu	Trp	Gly	Ala	Arg	Ala	Pro	Gly	Asn	Ala	Gln	Glu	Thr	
87					245					250						255	
89	agg	gac	gct	aac	cac	atg	cga	aac	aag	aag	gtg	ata	aaa	atg	ttg	816	
90	Arg	Asp	Ala	Asn	His	Met	Arg	Asn	Lys	Lys	Lys	Val	Ile	Lys	Met	Leu	
91					260					265						270	
93	gtg	ctg	gtc	gta	gct	ctg	ttt	gcf	tta	tgc	tgg	ctg	ccg	cta	cag	acg	864
94	Val	Leu	Val	Val	Ala	Leu	Phe	Ala	Leu	Cys	Trp	Leu	Pro	Leu	Gln	Ser	
95					275					280						285	
97	tac	tta	tta	cta	caa	tca	ttt	ttt	cca	tca	att	aat	gag	tac	aag	tac	912
98	Tyr	Leu	Leu	Gln	Ser	Phe	Phe	Pro	Ser	Ile	Asn	Glu	Tyr	Lys	Tyr		
99					290					295						300	
101	att	acc	aac	gtg	ctt	ttc	ttt	tgc	ttc	gac	tgg	cta	gca	atg	agc	aac	960
102	Ile	Asn	Val	Leu	Phe	Phe	Cys	Phe	Asp	Trp	Leu	Ala	Met	Ser	Asn	Ser	
103					305					310						315	320
105	tgc	tat	aac	cca	tcc	atc	tat	gcc	atc	tac	aac	gaa	aaa	ttc	aag	aag	1008
106	Cys	Tyr	Asn	Pro	Phe	Ile	Tyr	Ala	Ile	Tyr	Asn	Glu	Lys	Phe	Lys	Lys	
107					325					330						335	
109	gaa	ttc	aaa	caa	cga	tcc	act	ttc	ggg	aaa	aag	cca	agc	aga	ttc	gtt	1056
110	Glu	Phe	Lys	Gln	Arg	Phe	Thr	Phe	Gly	Lys	Lys	Pro	Ser	Arg	Phe	Val	
111					340					345						350	
113	aac	gat	agc	tac	gag	gac	ggc	cag	tca	tac	cga	aca	aga	att	tta	tcg	1104
114	Asn	Asp	Ser	Tyr	Glu	Asp	Gly	Gln	Ser	Tyr	Arg	Thr	Arg	Ile	Leu	Ser	
115					355					360						365	
117	ttc	cga	tca	acc	aac	gac	aga	agt	ggc	tat	tca	tcc	aga	aag	tct	ttg	1152
118	Phe	Arg	Ser	Thr	Asn	Asp	Arg	Ser	Gly	Tyr	Ser	Ser	Arg	Lys	Ser	Leu	
119					370					375						380	
121	aac	ata	ccg	ccg	ggg	gac	act	tta	aaa	gtt	cct	tct	aga	aat	tca	tgt	1200
122	Asn	Ile	Pro	Pro	Gly	Asp	Thr	Leu	Lys	Val	Pro	Ser	Arg	Asn	Ser	Cys	
123					385					390						395	400
125	cat	tgc	atg	gcf	aat	cag	agc	aga	gaa	aat	gga	ttt	aac	ttc	atg	aaa	1248

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126	His Cys Met Ala Asn Gln Ser Arg Glu Asn Gly Phe Asn Phe Met Lys			
127	405	410	415	
129	act gaa gac atg gaa ggg cac gga aat agc agg cgg tat ctg aat ata		1296	
130	Thr Glu Asp Met Glu Gly His Gly Asn Ser Arg Arg Tyr Leu Asn Ile			
131	420	425	430	
133	aga atg agt aat cca gat att ggt aaa aga aga tta gct aag aag tta		1344	
134	Arg Met Ser Asn Pro Asp Ile Gly Lys Arg Arg Leu Ala Lys Lys Leu			
135	435	440	445	
137	tgc aat aga gac gac atg cct ata ggt gat gag aga gtc agt gaa ctg		1392	
138	Ser Asn Arg Asp Asp Met Pro Ile Gly Asp Glu Arg Val Ser Glu Leu			
139	450	455	460	
141	tac ata ttc cca aac agt aac att gta gaa ttt aca gac ata tca tac		1440	
142	Tyr Ile Phe Pro Asn Ser Asn Ile Val Glu Phe Thr Asp Ile Ser Tyr			
143	465	470	475	480
145	gat gac aaa gtg		1452	
146	Asp Asp Lys Val			
150	<210> SEQ ID NO: 2			
151	<211> LENGTH: 484			
152	<212> TYPE: PRT			
153	<213> ORGANISM: Heliothis virescens			
155	<400> SEQUENCE: 2			
157	Met Asp Thr Ser Thr Thr Asn Ser Ser Gln Asp Asp Asp Ala Asp Trp			
158	1	5	10	15
161	Pro Arg Asn Ser Ser Ile Asp Glu Tyr Ile Ile His Asn Gly Thr Asn			
162	20	25	30	
165	Asp Thr Phe Glu Thr Leu Tyr Asp Val Pro Thr Gly Met Ile Val Leu			
166	35	40	45	
169	Leu Ser Phe Leu Tyr Gly Ser Ile Ser Val Leu Ala Val Val Gly Asn			
170	50	55	60	
173	Phe Leu Val Met Trp Val Val Ala Thr Ser Arg Arg Met Gln Ser Val			
174	65	70	75	80
177	Thr Asn Cys Tyr Ile Ala Asn Leu Ala Leu Ala Asp Ile Val Ile Gly			
178	85	90	95	
181	Leu Phe Ala Val Pro Phe Gln Phe Gln Ala Ala Leu Leu Gln Arg Trp			
182	100	105	110	
185	Leu Leu Pro His Phe Met Cys Pro Phe Cys Pro Phe Val Gln Ala Leu			
186	115	120	125	
189	Ser Val Asn Val Ser Val Phe Thr Leu Thr Ala Ile Ala Val Asp Arg			
190	130	135	140	
193	His Arg Ala Ile Ile Thr Pro Leu Ser Ala His Thr Ser Lys Arg Ile			
194	145	150	155	160
197	Ala Lys Val Ile Ile Val Val Ile Trp Phe Leu Ala Leu Ser Leu Ala			
198	165	170	175	
201	Ala Pro Met Ala Met Ser Trp Glu Val Ile Met Glu Asp Glu Leu Asp			
202	180	185	190	
205	Pro Val Ala Lys Ile Phe Tyr Lys Lys Pro Phe Cys Ala Pro Thr Glu			
206	195	200	205	
209	Phe Gly Ser His Ser Leu Ala Ile Tyr Arg Leu Leu Tyr Val Phe			
210	210	215	220	

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213 Gln Tyr Val Ile Pro Leu Cys Val Ile Thr Phe Ala Tyr Ala His Met  
214 225 230 235 240  
217 Ala Met Lys Leu Trp Gly Ala Arg Ala Pro Gly Asn Ala Gln Glu Thr  
218 245 250 255  
221 Arg Asp Ala Asn His Met Arg Asn Lys Lys Lys Val Ile Lys Met Leu  
222 260 265 270  
225 Val Leu Val Val Ala Leu Phe Ala Leu Cys Trp Leu Pro Leu Gln Ser  
226 275 280 285  
229 Tyr Leu Leu Leu Gln Ser Phe Phe Pro Ser Ile Asn Glu Tyr Lys Tyr  
230 290 295 300  
233 Ile Asn Val Leu Phe Phe Cys Phe Asp Trp Leu Ala Met Ser Asn Ser  
234 305 310 315 320  
237 Cys Tyr Asn Pro Phe Ile Tyr Ala Ile Tyr Asn Glu Lys Phe Lys Lys  
238 325 330 335  
241 Glu Phe Lys Gln Arg Phe Thr Phe Gly Lys Lys Pro Ser Arg Phe Val  
242 340 345 350  
245 Asn Asp Ser Tyr Glu Asp Gly Gln Ser Tyr Arg Thr Arg Ile Leu Ser  
246 355 360 365  
249 Phe Arg Ser Thr Asn Asp Arg Ser Gly Tyr Ser Ser Arg Lys Ser Leu  
250 370 375 380  
253 Asn Ile Pro Pro Gly Asp Thr Leu Lys Val Pro Ser Arg Asn Ser Cys  
254 385 390 395 400  
257 His Cys Met Ala Asn Gln Ser Arg Glu Asn Gly Phe Asn Phe Met Lys  
258 405 410 415  
261 Thr Glu Asp Met Glu Gly His Gly Asn Ser Arg Arg Tyr Leu Asn Ile  
262 420 425 430  
265 Arg Met Ser Asn Pro Asp Ile Gly Lys Arg Arg Leu Ala Lys Lys Leu  
266 435 440 445  
269 Ser Asn Arg Asp Asp Met Pro Ile Gly Asp Glu Arg Val Ser Glu Leu  
270 450 455 460  
273 Tyr Ile Phe Pro Asn Ser Asn Ile Val Glu Phe Thr Asp Ile Ser Tyr  
274 465 470 475 480  
277 Asp Asp Lys Val

**VERIFICATION SUMMARY**

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L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:24 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:21